Sequence 1: US6472518_8 Sequence 8 from Patent US 6472518 inClaims gi: 27289033
Length = 5416 (1 .. 5416)

Sequence 2: US20070219347_1 Sequence 1 Organism: Neisseria meningitidis
Length = 2242716 (1 .. 2242716)

Score = 8866 bits (4611), Expect = 0.0
 Identities = 4984/5076 (98%), Gaps = 42/5076 (0%)
 Strand=Plus/Plus

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Query  6       GCATGCAAGCTGGAAGGAAACTTGCCGCAGCCAGGAAAACGGTGCAGTGCAAGAGAGGGA   65
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Sbjct  436931  GCATGCAAGCTGGAAGGAAACTTGCCGCAGCC-GGAAAACGGTGCAGTGCAAGAGAGGGA   436989

Query  66      AGGGGGCGGCGGTTTGTTGGCAAGATTGAAACGGTGGATTGAAAACAGCTTCTGAACAGG   125
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  436990  AGGGGGCGGCGGTTTGTTGGCAAGATTGAAACGGTGGATTGAAAACAGCTTCTGAACAGG   437049

Query  126     TGGATTGCCGTTTGACAGGTGAGAAGTATTTTGCCAGCAGCAAGATACTTCTTATATAAT   185
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  437050  TGGATTGCCGTTTGACAGGTGAGAAGTATTTTGCCAGCAGCAAGATACTTCTTATATAAT   437109
                                                        → ORF1 BEGIN
Query  186     GAATAATAATTTATTTAAACCGTCCTCTGAATGGGGCGAGCAGGAGTTTTTGAATGGAAT   245
               ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Sbjct  437110  GAATAATAATTTATTTAAACCGTCCTCTGAATGGGGCGAGCAGGAGTTTTTGAATGGAAT   437169

Query  246     TTGTTTACGACGTGGCAGAATCGGCAGTCAGCCCTGCGGTGATTAAAGTAATCGGCTTGG   305
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  437170  TTGTTTACGACGTGGCAGAATCGGCAGTCAGCCCTGCGGTGATTAAAGTAATCGGCTTGG   437229

Query  306     GCGGCGGCGGTTGCAATGCATCCAATAACATGGTTGCCAACAATGTGCGCGGTGTGGAGT   365
               |||||||||||||||||||||||  |||||||||||||||||||||||||||||||||||
Sbjct  437230  GCGGCGGCGGTTGCAATGCAATCAATAACATGGTTGCCAACAATGTGCGCGGTGTGGAGT   437289

Query  366     TTATCAGTGCCAATACGGATGCGCAGTCTCTGGCAAAAAACCATGCGGCGAAGAGAATCC   425
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  437290  TTATCAGTGCCAATACGGATGCGCAGTCTCTGGCAAAAAACCATGCGGCGAAGAGAATCC   437349

Query  426     AGTTGGGTACGAATCTGACACGCGGTTTGGGCGCGGGCGCGAATCCCGATATCGGCCGTG   485
               |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Sbjct  437350  AGTTGGGTACGAATCTGACACGCGGTTTGGGCGCGGGCGCGAATCCCGATATCGGCCGTG   437409

Query  486     CGGCAGCCCAGGAAGACCGGGAAGCCATTGAAGAAGCCATTCGCGGTGCGAATATGCTGT   545
               ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Sbjct  437410  CGGCAGCCCAGGAAGACCGGGAAGCCATTGAAGAAGCCATTCGCGGTGCGAATATGCTGT   437469

Query  546     TTATCACGACCGGTATGGGCGGCGGTACCGGTACCGGTTCCGCGCCCGGTTGTTGCTGAGA   605
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Sbjct  437470  TTATCACGACCGGTATGGGCGGCGGTACCGGTACCGGTTCCGCGCCCGGTTGTTGCTGAGA   437529

Query  606     TTGCCAAGTCTTTGGGCATTCTGACCGTTGCCGTGGTTACCCGACCGTTCGCATATGAAG   665
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  437530  TTGCCAAGTCTTTGGGCATTCTGACCGTTGCCGTGGTTACCCGACCGTTCGCATATGAAG   437589

Query  666     GTAAGCGCGTCCATGTCGCACAGGCAGGGTTGGAACAGTTGAAAGAACACGTCGATTCGC   725
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  437590  GTAAGCGCGTCCATGTCGCACAGGCAGGGTTGGAACAGTTGAAAGAACACGTCGATTCGC   437649

Query  726     TGATTATCATCCCGAACGACAAACTGATGACTGCATTGGGTGAAGACGTAACGATGCGCG   785
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  437650  TGATTATCATCCCGAACGACAAACTGATGACTGCATTGGGTGAAGACGTAACGATGCGCG   437709

Query  786     AAGCCTTCCGTGCCGCCGACAATGTATTGCGCGATGCGGTCGCAGGCATTTCCGAAGTGG   845
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Sbjct  437710  AAGCCTTCCGTGCCGCCGACAATGTATTGCGCGATGCGGTCGCAGGCATTTCCGAAGTGG   437769

Query  846     TAACTTGCCCGAGCGAAATCATCAACCTCGACTTTGCCGACGTGAAAACCGTGATGAGCA   905
               |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  437770  TAACTTGCCCGAGCGAAATCATCAACCTCGACTTTGCCGACGTGAAAACCGTGATGAGCA   437829
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Query    906    ACCGCGGTATCGCTATGATGGGTTCGGGTTATGCCCAAGGTATCGACCGTGCGCGTATGG    965
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Sbjct  437830    ACCGCGGTATCGCTATGATGGGTTCGGGTTATGCCCAAGGTATCGACCGTGCGCGTATGG    437889

Query    966    CGACCGACCAGGCCATTTCCAGTCCGCTGCTGGACGATGTAACCTTGGACGGAGCGCGCG    1025
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Sbjct  437890    CGACCGACCAGGCCATTTCCAGTCCGCTGCTGGACGATGTAACCTTGGACGGAGCGCGCG    437949

Query   1026    GTGTGCTGGTCAATATTACGACTGCTCCGGGTTGCTTGAAAATGTCCGAGTTGTCCGAAG    1085
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Sbjct  437950    GTGTGCTGGTCAATATTACGACTGCTCCGGGTTGCTTGAAAATGTCCGAGTTGTCCGAAG    438009

Query   1086    TCATGAAAATCGTCAACCAAAGCGCGCATCCCGATTTGGAATGCAAATTCGGTGCTGCTG    1145
                ||||||||||||||||||||||||||||||||||||||||||| |||||||||| ||||||
Sbjct  438010    TCATGAAAATCGTCAACCAAAGCGCGCATCCCGATTTGGAATGCAAATTCGGTGCGGCTG    438069

Query   1146    AAGACGAGACCATGAGCGAAGATGCCATCCGGATTACCATTATCGCTACCGGTCTGAAAG    1205
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  438070    AAGACGAGACCATGAGCGAAGATGCCATCCGGATTACCATTATCGCTACCGGTCTGAAAG    438129

Query   1206    AAAAAGGCGCGGTCGATTTTGTTCCGGCAAGGGAGGTAGAAGCGGTTGCCCCGTCCAAAC    1265
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  438130    AAAAAGGCGCGGTCGATTTTGTTCCGGCAAGGGAGGTAGAAGCGGTTGCCCCGTCCAAAC    438189

Query   1266    AGGAGCAAAGCCACAATGTCGAAGGTA-GATCCGCACCAATCGCGGTATCCGCACGATGA    1324
                ||||||||||||||||||||||||||| | ||||||||||||||||||||||||||||||
Sbjct  438190    AGGAGCAAAGCCACAATGTCGAAGGTATGATCCGCACCAATCGCGGTATCCGCACGATGA    438249

Query   1325    ACCTTACCGCTGCGGATTTCGACAATCAGTCCGTACTTGACGAC-TTGAAATCCCTGCGA    1383
                ||||||||||||||||||||||||||||||||||||||||||||  ||||||||||||||
Sbjct  438250    ACCTTACCGCTGCGGATTTCGACAATCAGTCCGTACTTGACGACTTGAAATCCCTGCGA    438309

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Query   1384    TTTTGCGTCGTCAACACATTCAGACAAATAATGTGCTGTTTGCCCGTAAACCTGCTGCC    1443
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Sbjct  438310    TTTTGCGTCGTCAACACAATTCAGACAAATAATGTGCTGTTTGCCCGTAAACCTGCTGCC    438369

Query   1444    TCCCGAATCGGTTTGTCCGGTTTGGGAGGTATGTTTTTCAAGATGTTGCAATTTCGTACG    1503
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Sbjct  438370    TCCCGAATCGGTTTGTCCGGTTTGGGAGGTATGTTTTTCAAGATGTTGCAATTTCGTACG    438429

Query   1504    GTTTGCGGTCGGCGGATTCAGATTTTTCCACTTGATACAGACTTTCAGATATGGACACTT    1563
                ||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||
Sbjct  438430    GTTTGCGGTCGGCGGATTCAGATTTTTCCACTTGATACAGACTTTCAGATATGGACACTT    438489

Query   1564    CAAAACAAACACTGTTGGACGGGATTTTTAAGCTGAAGGCAAACGGTACGACGGTGCGTA    1623
                ||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Sbjct  438490    CAAAACAAACACTGTTGGACGGGATTTTTAAGCTGAAGGCAAACGGTACGACGGTGCGTA    438549

Query   1624    CCGAGTTGATGGCGGGTTTGACAACTTTTTTGACGATGTGCTACATCGTTAATCGTCAAC    1683
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  438550    CCGAGTTGATGGCGGGTTTGACAACTTTTTTGACGATGTGCTACATCGTT-ATCGTCAAC    438608

Query   1684    CCTCTGATTTTGGGCGAGACCGGCATGGATATGGGGGGCGGTATTCGTCGCTACCTGTATC    1743
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  438609    CCTCTGATTTTGGGCGAGACCGGCATGGATATGGGGGGCGGTATTCGTCGCTACCTGTATC    438668

Query   1744    GCGTCTGCCAATCGGCTGTTTTGTTATGGGTTTTGTCGGCAACTATCCGATTGCACTCGC    1803
                ||||||||  ||||||||||||||| ||||||||||||||||||||||||||||||||||
Sbjct  438669    GCGTCTGCC-ATCGGCTGTTTTGTTATGGGTTTTGTCGGCAACTATCCGATTGCACTCGC    438727

Query   1804    ACCGGGGATGGGGCTGAATGCCTATTTCACCTTTGCCGTCGTTAAGGGTATGGGC-TGCC    1862
                |||||||||||||||||||||||||||||||||||||||||||||||||||||  ||||
Sbjct  438728    ACCGGGGATGGGGCTGAATGCCTATTTCACCTTTGCCGTCGTTAAGGGTATGGGCCGTGCC    438787

                                                                 ORF2 BEGIN
Query   1863    TTGGCAGGTTGCGTTGGGTGCGGTGTTCATCTCCGGTCTGATTTTCATCCTGTTCAGCTT    1922
                ||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Sbjct  438788    TTGGCAGGTTGCGTTGGGTGCGGTGTTCATCTCCGGTCTGATTTTTATCCTGTTCAGCTT    438847

Query   1923    TTTTAAAGTCAGGGAAATGCT-GTCAACGCACTGCCTATGGGTTTGAAAATGTCGATTGC    1981
                |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Sbjct  438848    TTTTAAAGTCAGGGAAATGCTGGTCAACGCACTGCCTATGGGTTTGAAAATGTCGATTGC    438907
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Query   1982   TGCCGGTATCGGTTTGTTTTTGGCACTGATTTCCCTGAAAGGCGCAGGCCATTATCGTTG   2041
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Sbjct   438908  TGCCGGTATCGGTTTGTTTTTGGCACTGATTTCCCTGAAAGGCGCAGG-CATTATCGTTG   438966

Query   2042   CCAATCCGGCAACCTTGGTCGGTTTGGGCGATATTCATCAGCCGTCCGCGTTGTTGGCAC   2101
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Sbjct   438967  CCAATCCGGCAACCTTGGTCGGTTTGGGCGATATTCATCAGCCGTCCGCGTTGTTGGCAC   439026

Query   2102   TGTTCCGTTTTGCTATGGTGGTCGTATTGGGACATTTCCGCGTTCAAGGCGCAA-CATCA   2160
               |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct   439027  TGTTCGGTTTTGCTATGGTGGTCGTATTGGGACATTTCCGCGTTCAAGGCGCAATCATCA   439086

Query   2161   TCACCATCTTGACCATTACCGTCATTGCCAGCCTGATGGGTTTGAATGAATTTCACGGCA   2220
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   439087  TCACCATCTTGACCATTACCGTCATTGCCAGCCTGATGGGTTTGAATGAATTTCACGGCA   439146

Query   2221   TCATCGGCGAAGTACCGAGCATTGCGCCGACTTTTATGCAGATGGATTTTGAAGGCCTGT   2280
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Sbjct   439147  TCATCGGCGAAGTACCGAGCATTGCGCCGACTTTTATGCAGATGGATTTTGAAGGCCTGT   439206

Query   2281   TTACCGTCAGC-TGGTCA--GTGATTTTCGTCTTCTTCTTGGTCGATCTATTTGACAGTA   2337
               ||||||||||| |||||| ||||||||||| || ||||| |||||||||||||||||||
Sbjct   439207  TTACCGTCAGCATGGTCAGTGTGATTTTCGTCTTCTTCTTGGTCGATCTATTTGACAGTA   439266

Query   2338   CCGGAACGCTGGTCGGCATATCCCACCGTGCCGGGCTGCTGGTGGACGGTAAGCTGCCCC   2397
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   439267  CCGGAACGCTGGTCGGCATATCCCACCGTGCCGGGCTGCTGGTGGACGGTAAGCTGCCCC   439326

Query   2398   GCCTGAAACGCGCACTGCTTGCAGACTCTACCGCCATTATGGCAGGTGCGGCTTTGGGTA   2457
               ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Sbjct   439327  GCCTGAAACGCGCACTGCTTGCAGACTCTACCGCCATTGTGGCAGGTGCGGCTTTGGGTA   439386

Query   2458   CTTCTTCCACCACGCCTTATGTGGAAAGCGCGGCGGGCGTATCGGCAGGCGGACGGACCG   2517
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   439387  CTTCTTCCACCACGCCTTATGTGGAAAGCGCGGCGGGCGTATCGGCAGGCGGACGGACCG   439446

Query   2518   GCCTGACGGCGGTTACCGTCGGCGTATTGATGCTCGCCTGCCTGATGTTTTCACCTTTGG   2577
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   439447  GCCTGACGGCGGTTACCGTCGGCGTATTGATGCTCGCCTGCCTGATGTTTTCACCTTTGG   439506

Query   2578   CGAAAAGTGTTCCCGCTTTTGGCACCGCGCCCGCCCTGCTTTATGTCGGCACGCAGATGC   2637
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Sbjct   439507  CGAAAAGTGTTCCCGCTTTTGGCACCGCGCCCGCCCTGCTTTATGTCGGCACGCAGATGC   439566

Query   2638   TCCGCAGTGCGAGGGATATTGATTGGGACGATATGACGGAAGCCGCACCCGCATTCCTGA   2697
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Sbjct   439567  TCCGCAGTGCGAGGGATATTGATTGGGACGATATGACGGAAGCCGCACCTGCGTTCCTGA   439626

Query   2698   CCATTGTCTTCATGCCCGTTTACCTATTCGATTGCAGACGGCATCGCCTTCGGCTTCATCA   2757
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Sbjct   439627  CCATTGTTTTCATGCCCGTTTACTTATTCGATTGCAGACGGCATCGCTTTCGGCTTCATCA   439686

Query   2758   GCTATGCCGTGGTTAAACTTTTATGCCCGCCGCACCAAAGACGTTCCGCCTATGGAATGGG   2817
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Sbjct   439687  GTTATGCCGTGGTTAAACTTTTATGCCCGCCGCACCAAAGACGTTCCGCCTATGGTATCGA   439746

Query   2818   TTGTTGCCGTATTGTGGGCACTGAAATTCTGGTATTTGGGCTGATTGAATTCGATATTAAA   2877
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   439747  TTGTTGCCGTATTGTGGGCACTGAAATTCTGGTATTTGGGCTGATTGAATTCGATATTAAA   439806

Query   2878   AAGCCCGTCTGAAAGGTTTTCAGACGGCATTTTGTTTGCCGATATA-TTAATTTTTATTA   2936
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Sbjct   439807  AATGCCGTCTGAAAGGTTTTCAGACGGCATTTTGTTTGCCGATATATTTTAATTTTTATTA   439866

Query   2937   AATTATATAAAAATCAAATACATAATAAAAATACATCGGATTGCTTAAAAATAATACATTG   2996
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   439867  AATTATATAAAAATCAAATACATAATAAAAATACATCGGATTGCTTAAAAATAATACATTG   439926

Query   2997   TTTTTTTATGTATAAAAATATTTTATAAGTTTTCAGGATTTGGATTATTGAAAATTTTTCTT   3056
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ORF2 END

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Query   3057   GATTTCCTGACAATTTTATTGAAACAAATAATTCAAAATTAATCTAGTTTAATCATAGAA   3116
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Sbjct   439986 GATTTCCTGACAATTTTATTGAAACAAATAATTCAAAATTAATCTAGTTTAATCATGGAA   440045

Query   3117   TTAAAATAAAATATTAAAATTATGTAATGAGTCTCCTTAAAAATGTTTGACATTTTCAGT   3176
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Query   3177   CTTGTGTTTTAGATTATCGAAAAATAAAACTACATAACACTACAAAGGAATATTACTATG   3236
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Sbjct   440106 CTTGTGTTTTAGATTATCGAAAAATAAAACTACATAACACTACAAAGGAACATTACTATG   440165

Query   3237   AAACCAATTCAGATGTTTTCCCCTTTTCTGAATAATCCCCTTGTTTTCTTCTTGTCTGCG   3296
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Query   3297   GTTTTGCCGCATAATTCCGAACGGTCTGCTGTTTTTCTTTGATTCGTTTTAAATATCAAT   3356
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Sbjct   440226 GTTTTGCCGCATAATTCCGAACGGTCTGCTGTTTTTCTTTGATTCGTTTTAAATATCAAT   440285
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Query   3357   AAGATAATTTTTCCCATATATTTTAATGATTGGATTGGGATGCCCGACGCGTCGGATGG   3416
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Sbjct   440286 AAGATAATTTTTCCCATATATTTTAATGATTGGATTGGGATGCCCGACGCGTCGGATGG   440345

Query   3417   CTGTGTTTTGCCGTCCGAATGTGATGGAAGCCTGTCCATACTGAAAAAAAGTCTATAAAG   3476
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Sbjct   440346 CTGTGTTTTGCCGTCCGAATGTGATGGAAGCCTGTCCATACTGAAAAAAAGTCTATAAAG   440405

Query   3477   GAGAAATATGATGAGTCAACACTCTGCCGGAGCACGTTTCCGCCAAGCCGTGAAAGAATC   3536
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Sbjct   440406 GAGAAATATGATGAGTCAACACTCTGCCGGAGCACGTTTCCGCCAAGCCGTGAAAGAATC   440465

Query   3537   GAATCCGCTTGCCGTCGCCGGTTGCGTCAATGCTTATTTTGCACGATTGGCCACCCAAAG   3596
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   440466 GAATCCGCTTGCCGTCGCCGGTTGCGTCAATGCTTATTTTGCACGATTGGCCACCCAAAG   440525

Query   3597   CGGTTTCAAAGCCATCTATCTGTCTGGCGGCGGCGTGGCAGCCTGTTCTTGCGGTATCCC   3656
               ||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Sbjct   440526 CGGTTTCAAAGCCATCTATCTGTCTGGCGGCGGCGTGGCAGCCTGTTCTTGCGGTATCCC   440585

Query   3657   TGATTTGGGCATTACCACAATGGAAGATGTGCTGATCGACGCACGACGCATTACGGACAA   3716
               |||||||||| | |||||||||||||||||| |||||||||||||||||||||||||||||
Sbjct   440586 TGATTTGGGCATTACCACAATGGAAGATGTGCTGATCGACGCACGACGCATTACGGACAA   440645

Query   3717   CGTGGATNCGCCTCTGCTGGTGGACATCGATGTGGGTTGGGGCGGTGCATTCAATATTGC   3776
               ||||| | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   440646 CGTGGATACGCCTCTGCTGGTGGACATCGATGTGGGTTGGGGCGGTGCATTCAATATTGC   440705

Query   3777   CCGTACCATTCGCAACTTTGAACGCGCCGGTGTTGCAGCGGTTCACATCGAAGATCAGGT   3836
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   440706 CCGTACCATTCGCAACTTTGAACGCGCCGGTGTTGCAGCGGTTCACATCGAAGATCAGGT   440765
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Query   3837   AGCGCAAAAACGCTGCGGTCACCGTCCGAACAAAGCCATTGTTATCTNAAGATGNAATGG   3896
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Sbjct   440766 AGCGCAAAAACGCTGCGGCCACCGTCCGAACAAAGCCATTG-TATCTAAAGATGAAATGG   440824

Query   3897   TCGACCGTATCAAAGCTGCCGTAGATGCGCGCGTTGNTGNGAACTTCGTGATTATGGCGC   3956
               |||||||||||||||||||||||||||||||||||| || ||||||||||||||||||||
Sbjct   440825 TCGACCGTATCAAAGCTGCCGTAGATGCGCGCGTTGATGAGAACTTCGTGATTATGGCGC   440884

Query   3957   GTACCGATGCGCTGGCGGTAGAAGGTTTGGATGCCGCTATCGAACGCGCCCAAGCTTGTG   4016
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   440885 GTACCGATGCGCTGGCGGTAGAAGGTTTGGATGCCGCTATCGAACGCGCCCAAGCTTGTG   440944

Query   4017   TCGAAAGCCGGTGCGGACATGATTTTCCCTGAAGCCATGACCGATTTGAACATGTACCGC   4076
               ||| ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   440945 TCG-AAGCCGGTGCGGACATGATTTTCCCTGAAGCCATGACCGATTTGAACATGTACCGC   441003

Query   4077   CAATTTGCAGATGCGGTGAAAGTG--CGTGTTGGCGAACATTACCGAGTTTGGTTCCACT   4134
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Sbjct   441004 CAATTTGCAGATGCGGTGAAAGTGCCCGTGTTGGCGAACATTACCGAGTTTGGTTCCACT   441063
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Query  4135    CCGCTTTATACCCAAAGCGAGCTGGCTGAAAACGGCGTGTCGCTGGTGCTGTATCCGCTG    4194
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Sbjct  441064  CCGCTTTATACCCAAAGCGAGCTGGCTGAAAACGGCGTGTCGCTGGTGCTGTATCCGCTG    441123

Query  4195    TCATCGTTCCGTGCAGCAAGCAAAGCCGCTCTGAATGTTTACGAAGCGATTATGCGCGAT    4254
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  441124  TCATCGTTCCGTGCAGCAAGCAAAGCCGCTCTGAATGTTTACGAAGCGATTATGCGCGAT    441183

Query  4255    GGCACTCAGGCGGCGGTGGTGGACAGTATGCAAACCCGTGCCGAGCTGTACGAGCATCTG    4314
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  441184  GGCACTCAGGCGGCGGTGGTGGACAGTATGCAAACCCGTGCCGAGCTGTACGAGCATCTG    441243

Query  4315    AACTATCATGCCTTCGAGCAAAAACTGGATAAATTGTTTCAAAAATGATTTACCGCTTTC    4374
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  441244  AACTATCATGCCTTCGAGCAAAAACTGGATAAATTGTTTCAAAAATGATTTACCGCTTTC    441303

Query  4375    AGACGGTCTTTCAACAAATCCGCATCGGTCGTCTGAAAACCCGAAACCCATAAAAACACA    4434
               ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  441304  AGACTGCCTTTCAACAAATCCGCATCGGTCGTCTGAAAACCCGAAACCCATAAAAACACA    441363

Query  4435    AAGGAGAAATACCATGACTGAAACTACTCAAACCCCGACCTTCAAACCTAAGAAATCCGT    4494
               ||||||||||||||||||||||||||||||||||||||   |||||||| |||||||||||
Sbjct  441364  AAGGAGAAATACCATGACTGAAACTACTCAAACCCCGACCCTCAAACCTAAAAAATCCGT    441423

Query  4495    TGCGCTTTCAGGCGTTGCGGCCGGTAATACCGCTTTGTGTACCGTTGGCCGCACCCGGCA    4554
               |||||||| ||||||||||||||||||||||||||||||||||||||||||||    |||||
Sbjct  441424  TGCGCTTTCTGGCGTTGCGGCCGGTAATACCGCTTTGTGTACCGTTGGCCGTA-CCGGCA    441482

Query  4555    ACGATTTGGAGCTATCGCGGTTACGACATCTTGGATTTGGGCACAAAAATGC--GTTTGA    4612
               |||||||| ||||||||||||||||||||| ||||||||||||||||||||||  |||||||
Sbjct  441483  ACGATTT-GAGCTATCGCGGTTACGACATTCTGGATTT-GGCACAAAAATGCGAGTTTGA    441540

Query  4613    AGAAGTAGCCCACCTGCTGATTCACGGTCATCTGCCCAACAAATTCGACGTGGAAGCTTA    4672
               ||||| |||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Sbjct  441541  AGAAGTCGCCCACCTGCTGATTCACGGCCATCTGCCCCAACAAATTCGAGCTGGCCGCTTA    441600

Query  4673    TAAAAGGAAGCTCAAATCCATGCGCGGCCTGCCTATCCGTGT-ATTAAAGTTTTGGGAAA    4731
               ||||| |||||||||||||||||||||||||||||||||||| |||||||||   |||||
Sbjct  441601  TAAAACCAAGCTCAAATCCATGCGCGGCCTGCCTATCCGTGTGATTAAAGTTTT-GGAAA    441659

Query  4732    GCCTGCCTGCACATACCCATCCGGATGGACGGTAATGGCGTACCGGCGGTATTCCATGCTG    4791
               |||||||||||||||||||||||||| |||||  ||||| |||||||||| |||||||||||
Sbjct  441660  GCCTGCCTGCACATACCCATCC-GATGGAC-GTAAT-GCGTACCGGC-GTATCCATGCTG    441715

Query  4792    GGCTGCGTTCATCCCGAACGTGAAAGCCATCCCGGAAAGTGAAGCGCGCGACATCGCCGA    4851
               ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Sbjct  441716  GGCTGCGTTCATCCTGAACGTGAAAGCCAT-CCGGAAAGTGAAGCGCGCGACATCGCCGA    441774

Query  4852    CAAACTGATTG-CAGCCTCGG-AGCCTCCTGCTGTACTNGGTATCAATA-TCGCACAACG    4908
               |||||||||||  ||||||||| ||| ||||| |||||||||||||||| ||||||||||||
Sbjct  441775  CAAACTGATCGCCGCAGCCTCGGCAGCATCCTCTTGTACT-GGTATCAATATTCGCACAACG    441833

Query  4909    GCAAACGCATTGA-GTTG-AAGCGACG-AGAGA-CATCGGCGGTCATTTCCTGCAACTGT    4964
               |||||||||||||   ||||  ||||||| ||||| ||||||||||||||||||||||||||
Sbjct  441834  GCAAACGCATTGAGGTGTGAAAGCGACGACAGAGACATCGGCGGTCATTTCCTGCAACTGT    441893

Query  4965    TNCACGGC-AACGCCCAAGCG-ATCACACATCAAAGCCATGCACGTTTCACTGATTCTGT    5022
               | |||||| ||||||||||||| |||||||||||||||||||||||||||||||||  ||||
Sbjct  441894  TGCACGGCAAACGCCCAAGCGAATCACACATCAAAGCCATGCACGTTTCACTGATTCTGT    441953

Query  5023    ATG-CGAACACGAGTTCAACG-TTCTACCTTTACCG    5056
               |||  ||||||||||||||||| ||||||||||||||
Sbjct  441954  ATGCCGAACACGAGTTCAACGCTTCTACCTTTACCG    441989
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